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FIGURE 1

10 20 30 40 50 60 70
GTCGACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACCTTG CAGGGAGAAT AACTTGCGCA

80 90 100 110 120 130 140
CCCCACTTTG CGCCGGTGCC TTTGCCAG CGGAGCCTGC TTGCCATCT CCGAGCCCCA CCGCCCCCTCC

150 160 170 180 190 200 210
ACTCCTCGGC CTTGCCGAC ACTGAGACGC TGTTCCCAGC GTGAAAAGAG AGACTGCGCG GCCGGCACCC

220 230 240 250 260 270 280
GGGAGAAGGA GGAGGAAAG AAAAGGAACG GACATTGGT CCTTGCGCCA GGTCCCTTGGA CCAGAGTTT

290 300 310 320 330 340 350
TCCATGTGGA CGCTCTTCA ATGGACGTGT CCCCGCGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT

(1) 370 385 400
CGACC ATG GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC
MET Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Pro Gln Val

415 430 445
CTC CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC GCG
Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe Ala
(24)

460 475 490 505
GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC CTG AGC GAG
Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val Leu Ser Glu

520 535 550 565
TTC GAG TTG CGG CTG CTC AGC ATG TTC GGC CTG AAA CAG AGA CCC ACC CCC AGC
Phe Glu Leu Arg Leu Leu Ser MET Phe Gly Leu Lys Gln Arg Pro Thr Pro Ser

580 595 610
AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC CTG TAT CGC AGG CAC TCA GGT
Arg Asp Ala Val Val Pro Pro Tyr MET Leu Asp Leu Tyr Arg Arg His Ser Gly

625 640 655 670
CAG CCG GGC TCA CCC GCC CCA GAC CAC CGG TTG GAG AGG GCA GCC AGC CGA GCC
Gln Pro Gly Ser Pro Ala Pro Asp His Arg Leu Glu Arg Ala Ala Ser Arg Ala

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FIGURE 1 (CON'T)

685 700 715
AAC ACT GTG CGC AGC TTC CAC CAT GAA GAA TCT TTG GAA GAA CTA CCA GAA ACG
Asn Thr Val Arg Ser Phe His His Glu Glu Ser Leu Glu Leu Pro Glu Thr

730 745 760 775
AGT GGG AAA ACA ACC CGG AGA TTC TTC TTT AAT TTA AGT TCT ATC CCC ACG GAG
Ser Gly Lys Thr Thr Arg Arg Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu

790 805 820 835
GAG TTT ATC ACC TCA GCA GAG CTT CAG GTT TTC CGA GAA CAG ATG CAA GAT GCT
Glu Phe Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln MET Gln Asp Ala

850 865 880
TTA GGA AAC AAT AGC AGT TTC CAT CAC CGA ATT AAT ATT TAT GAA ATC ATA AAA
Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile Ile Lys

895 910 925 940
CCT GCA ACA GCC AAC TCG AAA TTC CCC GTG ACC AGA CTT TTG GAC ACC AGG TTG
Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu Asp Thr Arg Leu

955 970 985
GTG AAT CAG AAT GCA AGC AGG TGG GAA AGT TTT GAT GTC ACC CCC GCT GTG ATG
Val Asn Gln Asn Ala Ser Arg Trp Glu Ser Phe Asp Val Thr Pro Ala Val MET

1000 1015 1030 1045
CGG TGG ACT GCA CAG GGA CAC GCC AAC CAT GGA TTC GTG GTG GAA GTG GCC CAC
Arg Trp Thr Ala Gln Gly His Ala Asn His Gly Phe Val Val Glu Val Ala His

1060 1075 1090 1105
TTG GAG GAG AAA CAA GGT GTC TCC AAG AGA CAT GTT AGG ATA AGC AGG TCT TTG
Leu Glu Glu Lys Gln Gly Val Ser Lys Arg His Val Arg Ile Ser Arg Ser Leu
(249)

1120 1135 1150
CAC CAA GAT GAA CAC AGC TGG TCA CAG ATA AGG CCA TTG CTA GTA ACT TTT GGC
His Gln Asp Glu His Ser Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly
(266)

1165 1180 1195 1210
CAT GAT GGA AAA GGG CAT CCT CTC CAC AAA AGA GAA AAA CGT CAA GCC AAA CAC
His Asp Gly Lys Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His
(283)

1225 1240 1255
AAA CAG CGG AAA CGC CTT AAG TCC AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC
Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp
(296)

1270 1285 1300 1315
TTC AGT GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC GCC
Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala

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FIGURE 1 (CON'T)

1330 1345 1360 1375
TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG AAC TCC ACT
Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
1390 1405 1420
AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC TCT AAG ATT CCT AAG
Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys

1435 1450 1465 1480
GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC TCG ATG CTG TAC CTT GAC GAG
Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser MET Leu Tyr Leu Asp Glu

1495 1510 1525
AAT GAA AAG GTT GTA TTA AAG AAC TAT CAG GAC ATG GTT GTG GAG GGT TGT GGG
Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp MET Val Val Glu Gly Cys Gly

1540(396) 1553 1563 1573 1583 1593 1603
TGT CGC TAGTACAGCA AAATTAAATA CATAAATATA TATATATATA TATATTTAG AAAAAAGAAA
Cys Arg

AAAA

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FIGURE 2

10 20 30 40 50 60 70
CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCGC GGAGCCCGGC CCGGAAGCTA GGTGAGTGTG

80 90 100 110 120 130 140
GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG AGTATCTAGC TTGTCTCCCC

150 160 170 180 190 200 210
GATGGGATTC CCGTCCAAGC TATCTCGAGC CTGCAGCGCC ACAGTCCCCG GCCCTCGCCC AGGTTCACTG

220 230 240 250 260 270 280
CAACCGTTCA GAGGTCCCCA GGAGCTGCTG CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC

290 300 310 320 330 340 350
GTAGTGCCAT CCCGAGCAAC GCACTGCTGC AGCTCCCTG AGCCTTCCA GCAAGTTGT TCAAGATTGG

360 370 380 390 400 (1)
CTGTCAAGAA TCATGGACTG TTATTATATG CCTTGTTCG TGTCAAGACA CC ATG ATT CCT
MET Ile Pro

417 432 447 462
GGT AAC CGA ATG CTG ATG GTC GTT TTA TTA TGC CAA GTC CTG CTA GGA GGC GCG
Gly Asn Arg MET Leu MET Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly Ala

477 492 507
AGC CAT GCT AGT TTG ATA CCT GAG ACG GGG AAG AAA AAA GTC GCC GAG ATT CAG
Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys Lys Lys Val Ala Glu Ile Gln

522 537 552 567
GGC CAC GCG GGA GGA CGC CGC TCA GGG CAG AGC CAT GAG CTC CTG CGG GAC TTC
Gly His Ala Gly Arg Ser Gly Gln Ser His Glu Leu Leu Arg Asp Phe

582 597 612 627
GAG GCG ACA CTT CTG CAG ATG TTT GGG CTG CGC CGC CGC CCG CAG CCT AGC AAG
Glu Ala Thr Leu Leu Gln MET Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys

642 657 672
AGT GCC GTC ATT CCG GAC TAC ATG CGG GAT CTT TAC CGG CTT CAG TCT GGG GAG
Ser Ala Val Ile Pro Asp Tyr MET Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu

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FIGURE 2 (CON'T)

687 702 717 732
GAG GAG GAA GAG CAG ATC CAC AGC ACT GGT CTT GAG TAT CCT GAG CGC CCG GCC
Glu Glu Glu Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala

747 762 777
AGC CGG GCC AAC ACC GTG AGG AGC TTC CAC CAC GAA GAA CAT CTG GAG AAC ATC
Ser Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn Ile

792 807 822 837
CCA GGG ACC AGT GAA AAC TCT GCT TTT CGT TTC CTC TTT AAC CTC AGC AGC ATC
Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu Ser Ser Ile

852 867 882 897
CCT GAG AAC GAG GTG ATC TCC TCT GCA GAG CTT CGG CTC TTC CGG GAG CAG GTG
Pro Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu Phe Arg Glu Gln Val

912 927 942
GAC CAG GGC CCT GAT TGG GAA AGG GGC TTC CAC CGT ATA AAC ATT TAT GAG GTT
Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His Arg Ile Asn Ile Tyr Glu Val

957 972 987 1002
ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC ACA CGA CTA CTG GAC
MET Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile Thr Arg Leu Leu Asp

1017 1032 1047
ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG GAA ACT TTT GAT GTG AGC CCT
Thr Arg Leu Val His His Asn Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro

1062 1077 1092 1107
GCG GTC CTT CGC TGG ACC CCG GAG AAG CAG CCA AAC TAT GGG CTA GCC ATT GAG
Ala Val Leu Arg Trp Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu

1122 1137 1152 1167
GTG ACT CAC CTC CAT CAG ACT CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC
Val Thr His Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser

1182 1197 1212
CGA TCG TTA CCT CAA GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC
Arg Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val

1227 1242 1257 1272
ACC TTT GGC CAT GAT GGC CGG GGC CAT GCC TTG ACC CGA CGC CGG AGG GCC AAG
Thr Phe Gly His Asp Gly Arg His Ala Leu Thr Arg Arg Arg Arg Ala Lys

1287 1302 1317
CGT AGC CCT AAG CAT CAC TCA CAG CGG GCC AGG AAG AAG AAT AAG AAC TGC CGG
Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys Arg
(293)

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FIGURE 2 (CON'T)

1332 1347 1362 1377
CGC CAC TCG CTC TAT GTG GAC TTC AGC GAT GTG GGC TGG AAT GAC TGG ATT GTG
Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val

1392 1407 1422 1437
GCC CCA CCA GGC TAC CAG GCC TTC TAC TGC CAT GGG GAC TGC CCC TTT CCA CTG
Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp Cys Pro Phe Pro Leu

1452 1467 1482
GCT GAC CAC CTC AAC TCA ACC AAC CAT GCC ATT GTG CAG ACC CTG GTC AAT TCT
Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser

1497 1512 1527 1542
GTC AAT TCC AGT ATC CCC AAA GCC TGT TGT GTG CCC ACT GAA CTG AGT GCC ATC
Val Asn Ser Ser Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile

1557 1572 1587
TCC ATG CTG TAC CTG GAT GAG TAT GAT AAG GTG GTA CTG AAA AAT TAT CAG GAG
Ser MET Leu Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu

1602 1617 (408) 1636 1646 1656
ATG GTA GAG GGA TGT GGG TGC CGC TGAGATCAGG CAGTCCTTGA GGATAGACAG
MET Val Val Glu Gly Cys Gly Cys Arg

1666 1676 1686 1696 1706 1716 1726
ATATACACAC CACACACACA CACCACATAC ACCACACACA CACGTTCCCA TCCACTCACC CACACACTAC

1736 1746 1756 1766 1776 1786 1796
ACAGACTGCT TCCTTATAGC TGGACTTTA TTTAAAAAAA AAAAAAAA AATGGAAAAA ATCCCTAAC

1806 1816 1826 1836 1846 1856 1866
ATTCACCTTG ACCTTATTTA TGACTTTACG TGCAAATGTT TTGACCATAT TGATCATATA TTTGACAAA

1876 1886 1896 1906 1916 1926 1936
ATATATTTAT AACTACGTAT TAAAAGAAAA AAATAAAATG AGTCATTATT TTAAAAAAA AAAAAAAACT

1946
CTAGAGTCGA CGGAATTC

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FIGURE 3

10	20	30	40	50
GTGACCGAGC GGCGCGGACG GCCGCCTGCC CCCTCTGCCA CCTGGGGCGG				
60	70	80	90	99
TGCAGGGCCCG GAGCCCAG GCGGGTAGC GCGTAGAGCC GGCGCG ATG MET (1)				
108	117	126	135	144
CAC GTG CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG				
His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala				
153	162	171	180	189
CTC TGG GCA CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC				
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe				
198	207	216	225	234
AGC CTG GAC AAC GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC				
Ser Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu				
243	252	261	270	279
CGC AGC CAG GAG CGG CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT				
Arg Ser Gln Glu Arg Arg Glu MET Gln Arg Glu Ile Leu Ser Ile				
288	297	306	315	324
TTG GGC TTG CCC CAC CGC CCG CGC CCG CAC CTC CAG GGC AAG CAC				
Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His				
333	342	351	360	369
AAC TCG GCA CCC ATG TTC ATG CTG GAC CTG TAC AAC GCC ATG GCG				
Asn Ser Ala Pro MET Phe MET Leu Asp Leu Tyr Asn Ala MET Ala				
378	387	396	405	414
GTG GAG GAG GGC GGC GGG CCC GGC GGC CAG GGC TTC TCC TAC CCC				
Val Glu Glu Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro				
423	432	441	450	459
TAC AAG GCC GTC TTC AGT ACC CAG GGC CCC CCT CTG GCC AGC CTG				
Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu				
468	477	486	495	504
CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC ATG GTC ATG AGC TTC				
Gln Asp Ser His Phe Leu Thr Asp Ala Asp MET Val MET Ser Phe				
513	522	531	540	549
GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC CAC CCA CGC TAC				
Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro Arg Tyr				

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FIGURE 3 (Con't)

558	567	576	585	594
CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC CCA GAA GGG				
His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile Pro Glu Gly				
603	612	621	630	639
GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC TAC ATC				
Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Tyr Ile				
648	657	666	675	684
CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT CAG				
Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr Gln				
693	702	711	720	729
GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC				
Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu				
738	747	756	765	774
GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT				
Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe				
783	792	801	810	819
GAC ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC				
Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His				
828	837	846	855	864
AAC CTG GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC				
Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser				
873	882	891	900	909
ATC AAC CCC AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG				
Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln				
918	927	936	945	954
AAC AAG CAG CCC TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC				
Asn Lys Gln Pro Phe MET Val Ala Phe Phe Lys Ala Thr Glu Val				
963	972	981	990	999
CAC TTC CGC AGC ATC CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG				
His Phe Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln				
(293)				
1008	1017	1026	1035	1044
AAC CGC TCC AAG ACG CCC AAG AAC CAG GAA GCA GCC CTG CGG ATG GCC				
Asn Arg Ser Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg MET Ala				
1053	1062	1071	1080	1089
AAC GTG GCA GAG AAC AGC AGC AGC GAC CAG AGG CAG GCC TGT AAG				
Asn Val Ala Glu Asn Ser Ser Asp Gln Arg Gln Ala Cys Lys				

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FIGURE 3 (Con't)

1098 1107 1116 1125 1134
AAG CAC GAG CTG TAT GTC AGC TTC CGA GAC CTG GGC TGG CAG GAC
Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp

1143 1152 1161 1170 1179
TGG ATC ATC GCG CCT GAA GGC TAC GCC GCC TAC TAC TGT GAG GGG
Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly

1188 1197 1206 1215 1224
GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC ACC AAC CAC
Glu Cys Ala Phe Pro Leu Asn Ser Tyr MET Asn Ala Thr Asn His

1233 1242 1251 1260 1269
GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC CCG GAA ACG GTG
Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Ile Ser Val

1278 1287 1296 1305 1314
CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC GTC
Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val

1323 1332 1341 1350 1359
CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA TAC AGA
Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg

1368 1377 1386 1399
AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC
Asn MET Val Val Arg Ala Cys Gly Cys His
(431)

1409 1419 1429 1439 1448
GAGAATTCAAG ACCCTTGCGG GCCAAGTTTT TCTGGATCCT CCATTGCTC

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Figure 4

10 20 30 40 50
CGACCATGAG AGATAAGGAC TGAGGGCCAG GAAGGGGAAG CGAGCCCCGCC

60 70 80 90 100
GAGAGGTGGC GGGGACTGCT CACGCCAAGG GCCACAGCGG CCGCGCTCCG

110 120 130 140 150
GCCTCGCTCC GCCTCGCTCCAC GCCTCGCGGG ATCCCGCGGG GCAGCCCCGGC

159 168 177 186 195
CGGGCGGGGG ATG CCG GGG CTG GGG CGG AGG GCG CAG TGG CTG TGC
MET Pro Gly Leu Gly Arg Arg Ala Gln Trp Leu Cys
(1)

204 213 222 231 240
TGG TGG TGG GGG CTG CTG TGC AGC TGC TGC GGG CCC CCG CCG CTG
Trp Trp Trp Gly Leu Leu Cys Ser Cys Cys Gly Pro Pro Pro Leu

249 258 267 276 285
CGG CCG CCC TTG CCC GCT GCC GCG GCC GCC GCC GGG GGG CAG
Arg Pro Pro Leu Pro Ala Ala Ala Ala Ala Gly Gly Gln

294 303 312 321 330
CTG CTG GGG GAC GGC GGG AGC CCC GGC CGC ACG ACG GAG CAG CCG CCG
Leu Leu Gly Asp Gly Ser Pro Gly Arg Thr Glu Gln Pro Pro

339 348 357 366 375
CCG TCG CCG CAG TCC TCC TCG GGC TTC CTG TAC CGG CGG CTC AAG
Pro Ser Pro Gln Ser Ser Gly Phe Leu Tyr Arg Arg Leu Lys

384 393 402 411 420
ACG CAG GAG AAG CGG GAG ATG CAG AAG GAG ATC TTG TCG GTG CTG
Thr Gln Glu Lys Arg Glu MET Gln Lys Glu Ile Leu Ser Val Leu

429 438 447 456 465
GGG CTC CCG CAC CGG CCC CGG CCC CTG CAC GGC CTC CAA CAG CCG
Gly Leu Pro His Arg Pro Arg Pro Leu His Gly Leu Gln Gln Pro

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Figure 4 (Con't)

474 483 492 501 510
CAG CCC CCG GCG CTC CGG CAG CAG GAG GAG CAG CAG CAG CAG
Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu Gln Gln Gln Gln

519 528 537 546 555
CAG CTG CCT CGC GGA GAG CCC CCT CCC GGG CGA CTG AAG TCC GCG
Gln Leu Pro Arg Gly Glu Pro Pro Gly Arg Leu Lys Ser Ala

564 573 582 591 600
CCC CTC TTC ATG CTG GAT CTG TAC AAC GCC CTG TCC GCC GAC AAC
Pro Leu Phe MET Leu Asp Leu Tyr Asn Ala Leu Ser Ala Asp Asn

609 618 627 636 645
GAC GAG GAC GGG GCG TCG GAG GGG GAG AGG CAG CAG TCC TGG CCC
Asp Glu Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser Trp Pro

654 663 672 681 690
CAC GAA GCA GCC AGC TCG TCC CAG CGT CGG CAG CCG CCC CCG GGC
His Glu Ala Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Gly Ser

699 708 717 726 735
GCC GCG CAC CCG CTC AAC CGC AAG AGC CTT CTG GCC CCC GGA TCT
Pro Pro Gly Ala Ala His Pro Leu Asn Arg Lys Ser Leu Leu Ala

744 753 762 771 780
GGC AGC GGC GGC GCG TCC CCA CTG ACC AGC GCG CAG GAC AGC GCC
Gly Ser Gly Ala Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala

789 798 807 816 825
TTC CTC AAC GAC GCG GAC ATG GTC ATG AGC TTT GTG AAC CTG GTG
Phe Leu Asn Asp Ala Asp MET Val MET Ser Phe Val Asn Leu Val

834 843 852 861 870
GAG TAC GAC AAG GAG TTC TCC CCT CGT CAG CGA CAC CAC AAA GAG
Glu Tyr Asp Lys Glu Phe Ser Pro Arg Gln Arg His His Lys Glu

879 888 897 906 915
TTC AAG TTC AAC TTA TCC CAG ATT CCT GAG GGT GAG GTG GTG ACG
Phe Lys Phe Asn Leu Ser Gln Ile Pro Glu Gly Glu Val Val Thr

924 933 942 951 960
GCT GCA GAA TTC CGC ATC TAC AAG GAC TGT GTT ATG GGG AGT TTT
Phe Arg Ile Tyr Lys Asp Cys Val MET Ala Ala Glu Gly Ser Phe

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Figure 4 (Con't)

969 978 987 996 1005
AAA AAC CAA ACT TTT CTT ATC AGC ATT TAT CAA GTC TTA CAG GAG
Lys Asn Gln Thr Phe Leu Ile Ser Ile Tyr Gln Val Leu Gln Glu

1014 1023 1032 1041 1050
CAT CAG CAC AGA GAC TCT GAC CTG TTT TTG TTG GAC ACC CGT GTA
His Gln His Arg Asp Ser Asp Leu Phe Leu Leu Asp Thr Arg Val

1059 1068 1077 1086 1095
GTA TGG GCC TCA GAA GAA GGC TGG CTG GAA TTT GAC ATC ACG GCC
Val Trp Ala Ser Glu Glu Gly Trp Leu Glu Phe Asp Ile Thr Ala

1104 1113 1122 1131 1140
ACT AGC AAT CTG TGG GTT GTG ACT CCA CAG CAT AAC ATG GGG CTT
Thr Ser Asn Leu Trp Val Val Thr Pro Gln His Asn MET Gly Leu

1149 1158 1167 1176 1185
CAG CTG AGC GTG GTG ACA AGG GAT GGA GTC CAC GTC CAC CCC CGA
Gln Leu Ser Val Val Thr Arg Asp Gly Val His Val His Pro Arg

1194 1203 1212 1221 1230
GCC GCA GGC CTG GTG GGC AGA GAC GGC CCT TAC GAT AAG CAG CCC
Ala Ala Gly Leu Val Gly Arg Asp Gly Pro Tyr Asp Lys Gln Pro

1239 1248 1257 1266 1275
TTC ATG GTG GCT TTC TTC AAA GTG AGT GAG GTC CAC GTG CGC ACC
Phe MET Val Ala Phe Phe Lys Val Ser Glu Val His Val Arg Thr

1284 1293 1302 1311 1320
ACC AGG TCA GCC TCC AGC CGG CGC CGA CAA CAG AGT CGT AAT CGC
Thr Arg Ser Ala Ser Ser Arg Arg Gln Gln Ser Arg Asn Arg
(382)

1329 1338 1347 1356 1365
TCT ACC CAG TCC CAG GAC GTG GCG CGG GTC TCC AGT GCT TCA GAT
Ser Thr Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala Ser Asp
(388)

1374 1383 1392 1401 1410
TAC AAC AGC AGT GAA TTG AAA ACA GCC TGC AGG AAG CAT GAG CTG
Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu Leu
(412)

1419 1428 1437 1446 1455
TAT GTG AGT TTC CAA GAC CTG GGA TGG CAG GAC TGG ATC ATT GCA
Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala

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Figure 4 (Con't)

1464 1473 1482 1491 1500
CCC AAG GGC TAT GCT GCC AAT TAC TGT GAT GGA GAA TGC TCC TTC
Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe

1509 1518 1527 1536 1545
CCA CTC AAC GCA CAC ATG AAT GCA ACC AAC CAC GCG ATT GTG CAG
Pro Leu Asn Ala His MET Asn Ala Thr Asn His Ala Ile Val Gln

1554 1563 1572 1581 1590
ACC TTG GTT CAC CTT ATG AAC CCC GAG TAT GTC CCC AAA CCG TGC
Thr Leu Val His Leu MET Asn Pro Glu Tyr Val Pro Lys Pro Cys

1599 1608 1617 1626 1635
TGT GCG CCA ACT AAG CTA AAT GCC ATC TCG GTT CTT TAC TTT GAT
Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp

1644 1653 1662 1671 1680
GAC AAC TCC AAT GTC ATT CTG AAA AAA TAC AGG AAT ATG GTT GTA
Asp Asn Ser Asn Val Ile Leu Lys Tyr Arg Asn MET Val Val

1689 1698 1708 1718 1728
AGA GCT TGT GGA TGC CAC TAACTCGAAA CCAGATGCTG GGGACACACA
Arg Ala Cys Gly Cys His
(513)

1738 1748 1758 1768 1778
TTCTGCCCTTG GATTCCCTAGA TTACATCTGC CTTAAAAAAA CACGGAAGCA

1788 1798 1808 1818 1828
CAGTTGGAGG TGGGACGATG AGACTTTGAA ACTATCTCAT GCCAGTGCCT

1838 1848 1858 1868 1878
TATTACCCAG GAAGATTTA AAGGACCTCA TTAATAATTT GCTCACTTGG

1888 1898 1908 1918 1928
TAAATGACGT GAGTAGTTGT TGGTCTGTAG CAAGCTGAGT TTGGATGTCT

1938 1948 1958 1968 1978
GTAGCATAAG GTCTGGTAAC TGCAGAAACA TAACCGTCAA GCTCTTCCTA

1988 1998 2008 2018 2028
CCCTCCTCCC CCAAAACCC ACCAAAATTA GTTTAGCTG TAGATCAAGC

2038 2048 2058 2068 2078
TATTGGGGT GTTTGTTAGT AAATAGGGAA AATAATCTCA AAGGAGTTAA

2088 2098 2108 2118 2128
ATGTATTCTT GGCTAAAGGA TCAGCTGGTT CAGTACTGTC TATCAAAGGT

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Figure 4 (Con't)

2138 2148 2158 2168 2178
AGATTTACA GAGAACAGAA ATCGGGGAAG TGGGGGGAAC GCCTCTGTTTC

2188 2198 2208 2218 2228
AGTTCATTC CAGAAGTCCA CAGGACGCAC AGCCCAGGCC ACAGCCAGGG

2238 2248 2258 2268 2278
CTCCACGGGG CGCCCTTGTC TCAGTCATTG CTGTTGTATG TTCGTGCTGG

2288 2298 2308 2318 2328
AGTTTGTTG GTGTGAAAAT ACACTTATTT CAGCCAAAAC ATACCATTTC

2338 2348 2358 2368 2378
TACACCTCAA TCCTCCATTT GCTGTACTCT TTGCTAGTAC CAAAAGTAGA

2388 2398 2408 2418 2428
CTGATTACAC TGAGGTGAGG CTACAAGGGG TGTGTAACCG TGTAACACGT

2438 2448 2458 2468 2478
GAAGGCAGTG CTCACCTCTT CTTTACCAGA ACGGTTCTTT GACCAGCACA

2488 2498 2508 2518 2528
TTAACCTCTG GACTGCCGGC TCTAGTACCT TTTCAGTAAA GTGGTTCTCT

2538 2548 2558 2568 2578
GCCTTTTAC TATACAGCAT ACCACGCCAC AGGGTTAGAA CCAACGAAGA

2588 2598 2608 2618 2628
AAATAAAATG AGGGTGCCCA GCTTATAAGA ATGGTGTAG GGGGATGAGC

2638 2648 2658 2668 2678
ATGCTGTTA TGAACGGAAA TCATGATTTC CCTGTAGAAA GTGAGGCTCA

2688 2698 2708 2718 2728
GATTAAATTT TAGAATATTT TCTAAATGTC TTTTCACAA TCATGTGACT

2738 2748 2758 2768 2778
GGGAAGGCAA TTTCATACTA AACTGATTAA ATAATACATT TATAATCTAC

2788 2798 2808 2818 2828
AACTGTTGC ACTTACAGCT TTTTTGTAA ATATAAACTA TAATTTATTG

2838 2848 2858 2868 2878
TCTATTTTAT ATCTGTTTG CTGTGGCGTT GGGGGGGGGG CCGGGCTTT

2888 2898 2908 2918
GGGGGGGGGG GTTTGTTGG GGGGTGTCGT GGTGTGGCG GGC GG

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Figure 5

10 20 30 40 50
CTGGTATATT TGTGCCTGCT GGAGGTGGAA TTAACAGTAA GAAGGGAGAAA

60 70 80 90 100
GGGATTGAAT GGACTTACAG GAAGGGATTTC AAGTAAATTC AGGGAAACAC

110 120 130 140 150
ATTTACTTGAA ATAGTACAAC CTAGAGTATT ATTTCACACT AAGACGACAC

160 170 180 190 200
AAAAGATGTT AAAGTTATCA CCAAGCTGCC GGACAGATAT ATATTCCAAC

210 220 230 240 250
ACCAAGGTGC AGATCAGCAT AGATCTGTGA TTCAGAAATC AGGATTGTT

260 270 280 290 300
TTGGAAAGAG CTCAAGGGTT GAGAAGAACT CAAAAGCAAG TGAAGATTAC

310 320 330 340 350
TTTGGAAACT ACAGTTTATC AGAAGATCAA CTTTGCTAA TTCAAATACC

360 370 380 390 400
AAAGGCCTGA TTATCATAAAA TTCAATATAGG AATGCATAGG TCATCTGATC

410 420 430 440 450
AAATAATATT AGCCGTCTTC TGCTACATCA ATGCAGCAAA AACTCTAAC

460 470 480 490 500
AACTGTGGAT AATTGGAAAT CTGAGTTCA GCTTTCTTAG AAATAACTAC

510 520 530 540 550
TCTTGACATA TTCCAAAATA TTTAAAATAG GACAGGAAAA TCGGTGAGGA

560 570 580 590 600
TGTTGTGCTC AGAAATGTCA CTGTCATGAA AAATAGGTAA ATTTGTTTTT

610 620 630 640 650
TCAGCTACTG GGAAACTGTA CCTCCTAGAA CCTTAGGTTT TTTTTTTTTT

660 670 680 690 700
AAGAGGACAA GAAGGACTAA AAATATCAAC TTTTGCTTTT GGACAAAA

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Figure 5 (Con't)

701 710 719 728 737
ATG CAT CTG ACT GTA TTT TTA CTT AAG GGT ATT GTG GGT TTC CTC
MET His Leu Thr Val Phe Leu Leu Lys Gly Ile Val Gly Phe Leu
(1)

746 755 764 773 782
TGG AGC TGC TGG GTT CTA GTG GGT TAT GCA AAA GGA GGT TTG GGA
Trp Ser Cys Trp Val Leu Val Gly Tyr Ala Lys Gly Gly Leu Gly

791 800 809 818 827
GAC AAT CAT GTT CAC TCC AGT TTT ATT TAT AGA AGA CTA CGG AAC
Asp Asn His Val His Ser Ser Phe Ile Tyr Arg Arg Leu Arg Asn

836 845 854 863 872
CAC GAA AGA CGG GAA ATA CAA AGG GAA ATT CTC TCT ATC TTG GGT
His Glu Arg Arg Glu Ile Gln Arg Glu Ile Leu Ser Ile Leu Gly

881 890 899 908 917
TTG CCT CAC AGA CCC AGA CCA TTT TCA CCT GGA AAA ATG ACC AAT
Leu Pro His Arg Pro Arg Pro Phe Ser Pro Gly Lys Gln Ala Ser

926 935 944 953 962
CAA GCG TCC TCT GCA CCT CTC TTT ATG CTG GAT CTC TAC AAT GCC
Ser Ala Pro Leu Phe MET Leu Asp Leu Tyr Asn Ala MET Thr Asn

971 980 989 998 1007
GAA GAA AAT CCT GAA GAG TCG GAG TAC TCA GTA AGG GCA TCC TTG
Glu Glu Asn Pro Glu Glu Ser Glu Tyr Ser Val Arg Ala Ser Leu

1016 1025 1034 1043 1052
GCA GAA GAG ACC AGA GGG GCA AGA AAG GGA TAC CCA GCC TCT CCC
Ala Glu Glu Thr Arg Gly Ala Arg Lys Gly Tyr Pro Ala Ser Pro

1061 1070 1079 1088 1097
AAT GGG TAT CCT CGT CGC ATA CAG TTA TCT CGG ACG ACT CCT CTG
Asn Gly Tyr Pro Arg Arg Ile Gln Leu Ser Arg Thr Thr Pro Leu

1106 1115 1124 1133 1142
ACC ACC CAG AGT CCT CCT CTA GCC AGC CTC CAT GAT ACC AAC TTT
Thr Thr Gln Ser Pro Pro Leu Ala Ser Leu His Asp Thr Asn Phe

1151 1160 1169 1178 1187
CTG AAT GAT GCT GAC ATG GTC ATG AGC TTT GTC AAC TTA GTT GAA
Leu Asn Asp Ala Asp MET Val MET Ser Phe Val Asn Leu Val Glu

1196 1205 1214 1223 1232
AGA GAC AAG GAT TTT TCT CAC CAG CGA AGG CAT TAC AAA GAA TTT
Arg Asp Lys Asp Phe Ser His Gln Arg Arg His Tyr Lys Glu Phe

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Figure 5 (con't)

1241 1250 1259 1268 1277
CGA TTT GAT CTT ACC CAA ATT CCT CAT GGA GAG GCA GTG ACA GCA
Arg Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala Val Thr Ala

1286 1295 1304 1313 1322
GCT GAA TTC CGG ATA TAC AAG GAC CGG AGC AAC AAC CGA TTT GAA
Ala Glu Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg Phe Glu

1331 1340 1349 1358 1367
AAT GAA ACA ATT AAG ATT AGC ATA TAT CAA ATC ATC AAG GAA TAC
Asn Glu Thr Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu Tyr

1376 1385 1394 1403 1412
ACA AAT AGG GAT GCA GAT CTG TTC TTG TTA GAC ACA AGA AAG GCC
Thr Asn Arg Asp Ala Asp Leu Phe Leu Leu Asp Thr Arg Lys Ala

1421 1430 1439 1448 1457
CAA GCT TTA GAT GTG GGT TGG CTT GTC TTT GAT ATC ACT GTG ACC
Gln Ala Leu Asp Val Gly Trp Leu Val Phe Asp Ile Thr Val Thr

1466 1475 1484 1493 1502
AGC AAT CAT TGG GTG ATT AAT CCC CAG AAT AAT TTG GGC TTA CAG
Ser Asn His Trp Val Ile Asn Pro Gln Asn Asn Leu Gly Leu Gln

1511 1520 1529 1538 1547
CTC TGT GCA GAA ACA GGG GAT GGA CGC AGT ATC AAC GTA AAA TCT
Leu Cys Ala Glu Thr Gly Asp Gly Arg Ser Ile Asn Val Lys Ser

1556 1565 1574 1583 1592
GCT GGT CTT GTG GGA AGA CAG GGA CCT CAG TCA AAA CAA CCA TTC
Ala Gly Leu Val Gly Arg Gln Gly Pro Gln Ser Lys Gln Pro Phe

1601 1610 1619 1628 1637
ATG GTG GCC TTC TTC AAG GCG AGT GAG GTA CTT CTT CGA TCC GTG
MET Val Ala Phe Phe Lys Ala Ser Glu Val Leu Leu Arg Ser Val

1646 1655 1664 1673 1682
AGA GCA GCC AAC AAA CGA AAA AAT CAA AAC CGC AAT AAA TCC AGC
Arg Ala Ala Asn Lys Arg Lys Asn Gln Asn Arg Asn Lys Ser Ser
(329)

1691 1700 1709 1718 1727
TCT CAT CAG GAC TCC TCC AGA ATG TCC AGT GTT GGA GAT TAT AAC
Ser His Gln Asp Ser Ser Arg MET Ser Ser Val Gly Asp Tyr Asn
(337)

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Figure 5 (Con't)

1736 1745 1754 1763 1772
ACA AGT GAG CAA AAA CAA GCC TGT AAG AAG CAC GAA CTC TAT GTG
Thr Ser Glu Gln Lys Gln Ala Cys Lys His Glu Leu Tyr Val
(356)

1781 1790 1799 1808 1817
AGC TTC CGG GAT CTG GGA TGG CAG GAC TGG ATT ATA GCA CCA GAA
Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
(362)

1826 1835 1844 1853 1862
GGA TAC GCT GCA TTT TAT TGT GAT GGA GAA TGT TCT TTT CCA CTT
Gly Tyr Ala Ala Phe Tyr Cys Asp Gly Glu Cys Ser Phe Pro Leu

1871 1880 1889 1898 1907
AAC GCC CAT ATG AAT GCC ACC AAC CAC GCT ATA GTT CAG ACT CTG
Asn Ala His MET Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu

1916 1925 1934 1943 1952
GTT CAT CTG ATG TTT CCT GAC CAC GTA CCA AAG CCT TGT TGT GCT
Val His Leu MET Phe Pro Asp His Val Pro Lys Pro Cys Cys Ala

1961 1970 1979 1988 1997
CCA ACC AAA TTA AAT GCC ATC TCT GTT CTG TAC TTT GAT GAC AGC
Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser

2006 2015 2024 2033 2042
TCC AAT GTC ATT TTG AAA AAA TAT AGA AAT ATG GTA GTA CGC TCA
Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn MET Val Val Arg Ser

2051 2060 2070 2080 2090 2100
TGT GGC TGC CAC TAATATTAAA TAATATTGAT AATAACAAAA AGATCTGTAT
Cys Gly Cys His
(454)

2110 2120 2130 2140 2150
TAAGGTTTAT GGCTGCAATA AAAAGCATAC TTTCAGACAA ACAGAAAAAA AAA

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Figure 6

(1)
GAATTCC GAG CCC CAT TGG AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT
Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala
(10)

GGG GAG GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC
Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His
(20) (30)

CTG CTC AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC
Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser
(40) (50)

AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT GGA GAC
Asn Arg Glu Ser Asp Leu Phe Leu Asp Leu Gln Thr Leu Arg Ala Gly Asp
(60) (70)

GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC TGG TTG CTG AAG
Glu Gly Typ Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cyc Trp Leu Leu Lys
(80)

CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG ACT GAG GAT GGG CAC AGC
Arg His Lys Asp Leu Gly Lue Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser
(90) (100)

GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT CAA CGG GCC CCA CGC TCC CAA CAG
Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln
(110) (120)

CCT TTC GTG GTC ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG
Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg
(130) (140)

GCA GTG AGG CCA CTG AGG AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG
Ala Val Arg Pro Leu Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln
(150) (160)

GCC AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CGG CAG
Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln
(170)

GTC TGC CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTT GGC TGG CTG GAC
Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp
(180) (190)

TGG GTC ATC GCC CCC CAA GGC TAC TCA GCC TAT TAC TGT GAG GGG GAG TGC TCC
Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser
(200) (210)

TTC CCG CTG GAC TCC TGC ATG AAC GCC ACC AAC CAC GGC ATC CTG CAG TCC CTG
Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu
(220) (230)

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Figure 6 (Con't)

G TG CAC CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC AAG
Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys
(240) (250)

CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC AGC AGC AAC AAC GTC ATC CTG CGC
Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg
(260)

AAG CAC CGC AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC TGAGTCAGCCCCCCCAGC
Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His
(270) (280)

CCTACTGCAGCCACCCTTCTCATCTGGATCGGGCCCTGCAGAGGCAGAAAACCCTAAATGCTGTCACAG
CTCAAGCAGGAGTGTCAAGGGGCCCTCACTCTCGGTGCCTACTTCCTGTCAGGCTCTGGGAATT

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FIGURE 7

GACGAAGGG CCTCGTGTATA CGOCTATTT TATAGGTTAA TGTCAATGATA ATAATGGTT 60
CTTAGACGTC AGGTGGCACT TTTCGGGAA ATGTGGCGGG AACCCGTATT TGTTTATTT 120
TCTAAATACA TTCAAATATA TATCCGCTCA TGAGACATA ACCGTATAA ATGCCCTCAAT 180
AATATTGAAA AAGGAAAGACT ATGAGTATTC AACATTTCCG TGTGGCCCTT ATTCCCTTT 240
TTGGGGCATT TTGGCTTCT GTTTTGCTC ACCGAGAAC GCTGGTGAAA GTAAAAGATG 300
CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAAGA 360
TCCTTGAGAG TTTTCGCCCC GAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC 420
TATGTGGCCG GGTATTATCC CGTATTGACC CGGGCARGA GCAACTCGT CGCCGCAATAC 480
ACTATTCTCA GAATGACTTG GTTGAGTACT CACCACTCAC AGAAAAGCAT CTTACGGATG 520
GGATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGGGGCCA 600
ACTTACTTCT GACAAACGATC CGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAAACATGG 660
GGGATCATGT AACTCGCCCT GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG 720
ACGAGCGTGA CACCAACGATG CCTGTAGCAA TGGCAACAAAC GTTGGCRAAA CTATTACTG 780
GCCGAACACT TACTCTAGCT TCCCGGCAAC AATTAAATAGA CTGGATGGAG GCGGATAAAG 840
TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAATCTG 900
GAGCCCGTGA CGCTGGGTCT CGCGGTATCA TTGAGGACT CGGGCCAGAT GGTAAGCCG 960
CCCGTATCGT AGTTATCTAC ACGACGGGAA GTCAGGCAAC TATGGATGAA CGAAATAGAC 1020
AGATCGCTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAAGAC CAAGTTACT 1080
CATATATACT TTAGATTGAT TTAAAACITC ATTTTTAATT TAAAGGATC TAGGTGAAGA 1140
TCCTTTTGA TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTTGTTC CACTGACCGT 1200
CAGACCCCGT AGAAAAAGTC AAAGGATCTT CTGAGGATCC TTTTTTTCTG CGCGTAATCT 1260
GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGG 1320
TACCAACTCT TTTTCCGAAG GTAACTGGCT TCAGCAGAGC GCAGATAACCA AATACTGTCC 1380
TTCTAGTGTG GCCGTAGTTA CGCCACCACT TCAAGAATCTC TGTAGCACCG COTACATACC 1440
TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG 1500
GGTTGGACTC AAGACGATAG TTACCCGATA AGCCCGACGG CGCGGGCTGA ACGGGGGGTT 1560
CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG 1620
AGCATTGAGA AAGCGCCACG CTTCOCGAAG CGAGAAAGGC CGACAGGTAT CGGGTAAGCG 1680
CGAGGGTCCG AAGAGGAGAG CGCACCGAGGG AGCTTCCAGG GGGAAACGCC TGTTATCTT 1740
ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGGCTCG ATTTTTGTGA TGCTCGTCAG 1800
GGGGGGGGAG CCTATGGAAA AACCCAGCA AGCGGGCCCTT TTTACGGTTC CTGGCCCTTT 1860
GCTGGCCTTT TGCTCACATO TTCTTCCCTG CGTTATCCCC TGATTCTGTO GATAACCGTA 1920

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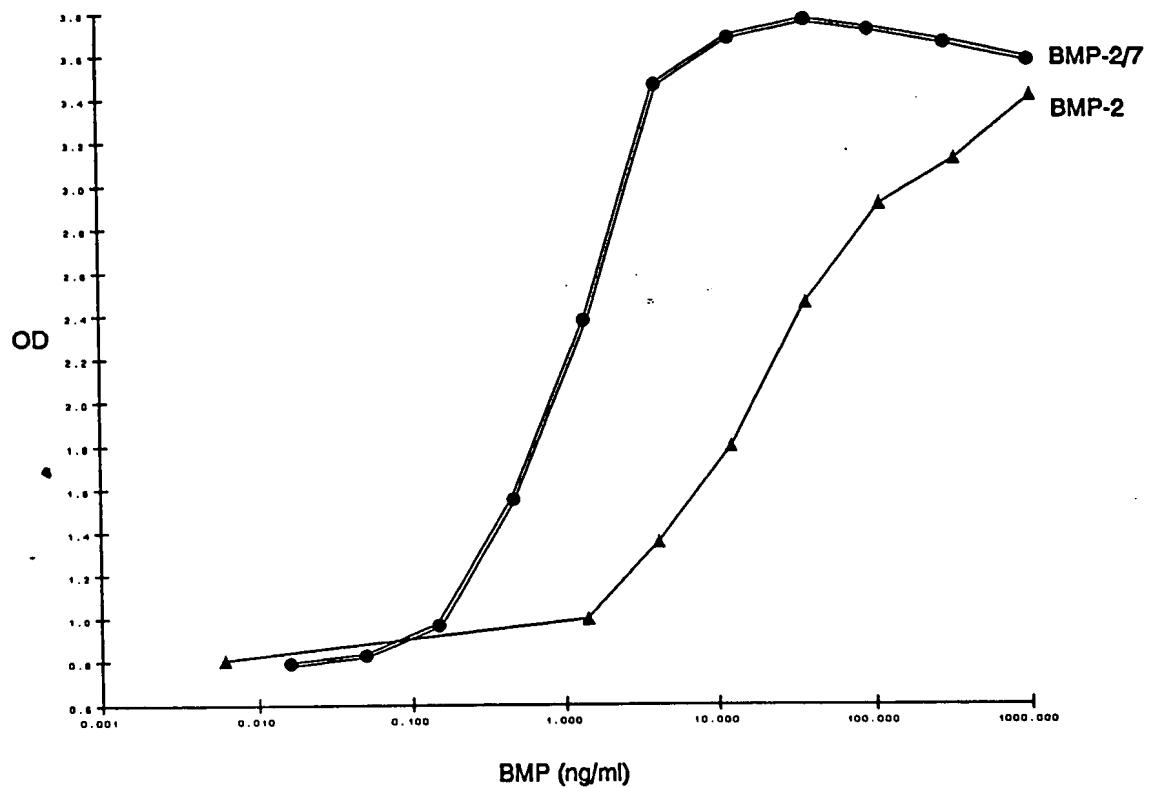
FIGURE 7 (cont'd)

TTACGGCTT TCACTGAGCT GATACCGCTC GCGCGAGCCG AACGACCGAG CGCAGCGAGT 1980
CACTGAGCGA CGRAGCGGA GAGCGCGAA TACCGAACCC GCCTCTCCCC GCGCGTTGGC 2040
CGATTGATTA ATGCAGAATT GATCTCTCAC CTACCAAACA ATGCCCTCCGT GCAAAAAATA 2100
AATTCAATA AAAAACATAC AGATAACCCT CTGCGGTGAT AAATTATCTC TGGCGGTGTT 2160
GACATAATA CGACTGGCGG TGATACTGAG CACATCAGCA GGACGGACTG ACCACCATGA 2220
AGCTGACGCT CTTAAAAATT AAGCCGTAA GAAAGGGCAGC ATTCAAAGCA GAGGGTTTG 2280
GGGTGTGTGA TACGAAACGA AGCATTGGC GTAAGTCGGA TTCCGGATTA GCTGGCAATG 2340
TCCCAATOGC GGGGGGTTT CGTTCAAGGAC TACAACTGCC ACACACCACCC AAAGCTTAATC 2400
GACAGGAGAA TCCAGATGGA TGCAAAACA CGCCGGCGCG AACGTCGCGC AGAGAAACAG 2460
GCTCAATGGA AAGCAGCAAA TCCCCGTGTTG GTTGGGTAA GCGAAAAACCC AGTTCCGAAA 2520
GATTTTTTA ACTATAAACG CTGATGGAG CGTTTATGGG GAAAGAGGTAA AGCCCTTCCC 2580
GAGTAACAAA AAAACAAACAG CATAAATAAC CCCGCTCTTA CACATTCCAG CCCTGAAAAA 2640
GGGCATCAAA TTAAACCRCA CCTATGGTGT ATGCATTTAT TTGCATACAT TCAATCAATT 2700
GTTATCTAAG GAAATACTTA CATATGGAG CTAACATAA ACAACGTAAA CGTCTGAATT 2760
CTAGCTGTAA GAGACACCCCT TTGTACGTGG ACTTCAGTGA CGTGGGGTGG AATGACTGGA 2820
TTGTGGCTCC CCCGGGTAT CACGCCCTTT ACTGCCACGG AGARTGCCCT TTTCCCTCTGG 2880
CTGATCATCT GAACTCCACT AATCATGCCA TTGTTCAAGAC GTGGTCAAC TCTGTTAACT 2940
CTAAGATTCC TAAGGCATGC TGTGTCGGCA CAGAACTCAQ TGCTATCTCG ATGCTGTACCC 3000
TTGACGAGAA TGAAAAGGT GTATTAAGA ACTATCAGGA CATGGTTGTG GAGGGTTGTG 3060
GGTGTGCTA GTACAGCAAA ATTAATAACA TAAATATATA TATATATATA TATTTAGAA 3120
AAAAGAAAAA AATCTAGAGT CGACCTGCAG TAATCGTACA GGGTAGTACA AATAAAAAAG 3180
GCACGGTCAGA TGACGGCCT TTTTCTTGT GAGCAGTAAG CTTGGCACTG GCCGTCGTTT 3240
TACAACGGTCG TGACTGGAA AACCCCTGGCG TTACCCAACT TAATCGCCTT GCAGCACATC 3300
CCCCTTTCGG CAGCTGGCGT AATAGCGAAG AGGCCCCAC CGATGCCCT TCCCAACAGT 3360
TGCGCAGCCT GAATGGCGAA TGGCGGCTGA TGGCGTATTT TCTCCTTACG CATCTGTGCG 3420
GTATTTCACA CCGCATATAT GGTGCACTCT CAGTACAATC TGCTCTGATG CGCGATAGTT 3480
AAGCCAGCCC CGACACCCCGC CAACACCCCGC TGACCGCGCC TGACGGGCTT GTCTGCTCCC 3540
GGCATCCGCT TACAGACAAG CTGTGACCGT CTGGGGGAGC TGCATGTOTC AGAGGTTTTC 3600
ACCGTCATCA CCGAAACCGG CGA

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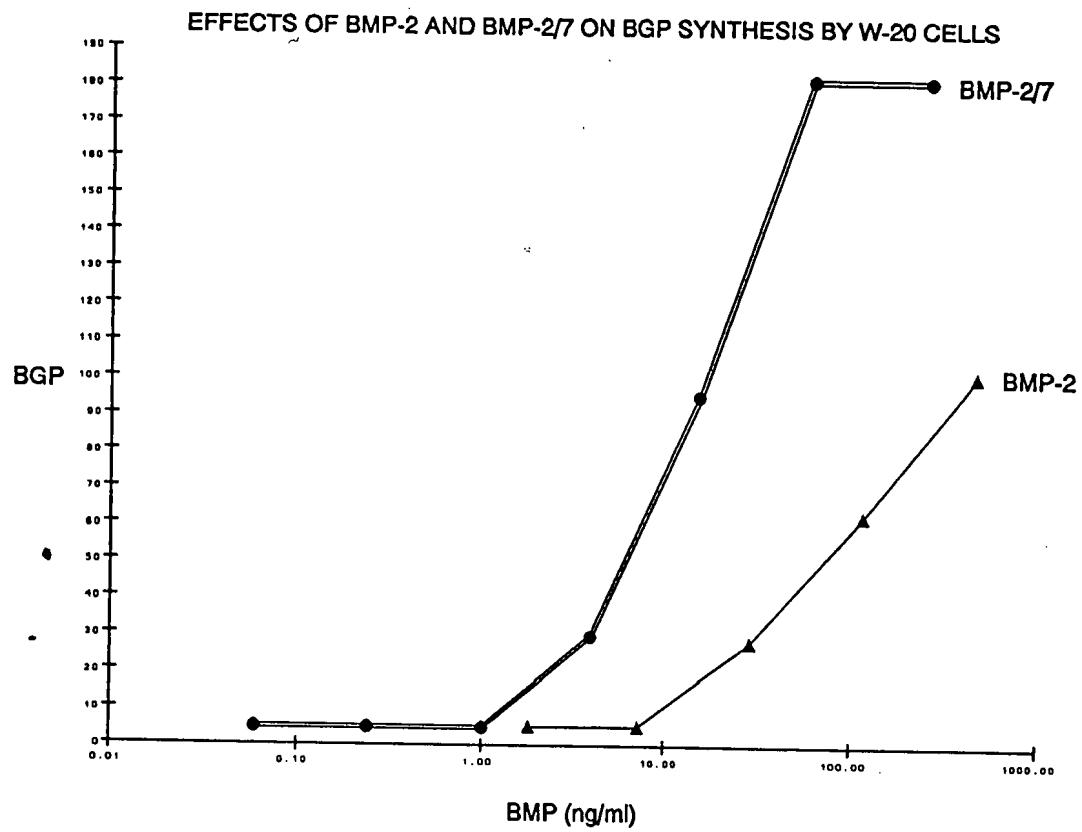
FIGURE 8

W-20 ALKALINE PHOSPHATASE: BMP-2 vs. BMP-2/7



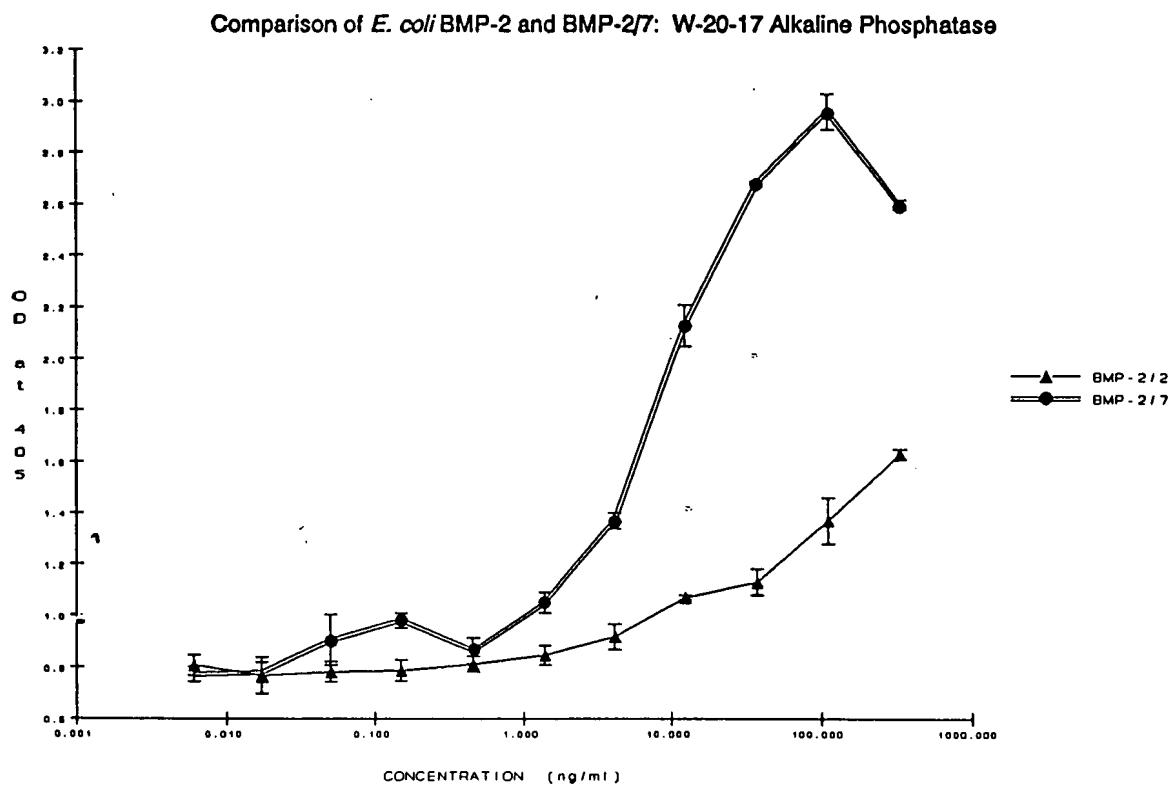
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FIGURE 9



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FIGURE 10



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FIGURE 11

10 20 30 40 50 60 70
AGATCITGAA AACACOOGGG CCACACAOGC OGOGACCTAC AGCTCTTCT CAGCGTTGGA GTGGAGAOGG

80 90 100 110 120 130 140
CGCCCOGCAGC GCGCTGOGOG GGTGAGGTOC GOGCAGCTGC TGGGAAAGAG CGACCCCTGTC AGGCTGCGCT

150 160 170 180 190 200 210
GGGTCAAGOGC AGCAAGTGGG GCTGGCOGCT ATCTCGCTGC ACGCGGCGC GTCCCGGGCT CGTGTGCCCG

220 230 240 250 260 270 280
TOGCCCGCAGC TGGTTTGGAG TTCAACOCTC GGCTOOGCGC CGGGCTCGTT GCGCTTTCGG AGTGTCCCCG

290 300 310 320 (1) 335
AGOGAOGCGCG GGAGOOGAOG CGCGOGOGGG GTACCTAGCC ATG GCT GGG CGG AGC AGG CTG CTC
MET Ala Gly Ala Ser Arg Leu Leu

350 365 380 395
TTT CTG TGG CTG GGC TGC TTC TGC GTG AGC CTG GCG CAG GGA GAG AGA CGG AAG CCA
Phe Leu Trp Leu Gly Cys Phe Cys Val Ser Leu Ala Gln Gly Glu Arg Pro Lys Pro

410 425 440 455
CGT TTC CGG GAG CTC CGC AAA GCT GTG CCA GGT GAC CGC ACG GCA GGT GGT CGG CGG
Pro Phe Pro Glu Leu Arg Lys Ala Val Pro Gly Asp Arg Thr Ala Gly Gly Pro

470 485 500 515
GAC TCC GAG CTG CAG CGG CAA GAC AAG GTC TCT GAA CAC ATG CTG CGG CTC TAT GAC
Asp Ser Glu Leu Gln Pro Gln Asp Lys Val Ser Glu His MET Leu Arg Leu Tyr Asp

530 545 560
AGG TAC AGC ACG GTC CAG CGG GCC CGG ACA CGG GGC TCC CTG GAG GGA GGC TOG CAG
Arg Tyr Ser Thr Val Gln Ala Ala Arg Thr Pro Gly Ser Leu Glu Gly Ser Gln

575 590 605 620
CCC TGG CGC CCT CGG CTC CTG CGC GAA GGC AAC ACG GTT CGC AGC TTT CGG CGG GCA
Pro Trp Arg Pro Arg Leu Leu Arg Glu Gly Asn Thr Val Arg Ser Phe Arg Ala Ala

635 650 665 680
GCA GCA GAA ACT CTT GAA AGA AAA GGA CTG TAT ATC TTC AAT CTG ACA TOG CTA ACC
Ala Ala Glu Thr Leu Glu Arg Lys Gly Leu Tyr Ile Phe Asn Leu Thr Ser Leu Thr

695 710 725 740
AAG TCT GAA AAC ATT TTG TCT GCC ACA CTG TAT TTC TGT ATT GGA GAG CTA GGA AAC
Lys Ser Glu Asn Ile Leu Ser Ala Thr Leu Tyr Phe Cys Ile Gly Glu Leu Gly Asn

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FIGURE 11 (Continued)

755 770 785 800
ATC AGC CTG AGT TGT CCA GTG TCT GGA GGA TGC TCC CAT CAT GCT CAG AGG AAA CAC
Ile Ser Leu Ser Cys Pro Val Ser Gly Gly Cys Ser His His Ala Gln Arg Lys His

815 830 845
ATT CAG ATT GAT CTT TCT GCA TGG ACC CTC AAA TTC AGC AGA AAC CAA AGT CAA CTC
Ile Gln Ile Asp Leu Ser Ala Trp Thr Leu Lys Phe Ser Arg Asn Gln Ser Gln Leu

860 875 890 905
CIT GGC CAT CTG TCA GTG GAT ATG GCC AAA TCT CAT CGA GAT ATT ATG TCC TGG CTG
Leu Gly His Leu Ser Val Asp MET Ala Lys Ser His Arg Asp Ile MET Ser Trp Leu

920 935 950 965
TCT AAA GAT ATC ACT CAA TTC TTG AGG AAG GCC AAA GAA AAT GAA GAG TTC CTC ATA
Ser Lys Asp Ile Thr Gln Phe Leu Arg Lys Ala Lys Glu Asn Glu Glu Phe Leu Ile

980 995 1010 1025
GGA TTT AAC ATT ACG TCC AAG GGA CGC CAG CTG CCA AAG AGG AGG TTA CCT TTT CCA
Gly Phe Asn Ile Thr Ser Lys Gly Arg Gln Leu Pro Lys Arg Arg Leu Pro Phe Pro

1040 1055 1070 1085
GAG CCT TAT ATC TTG GTA TAT GCC AAT GAT GCC GCC ATT TCT GAG CCA GAA AGT GTG
Glu Pro Tyr Ile Leu Val Tyr Ala Asn Asp Ala Ala Ile Ser Glu Pro Glu Ser Val

1100 1115 1130
GTA TCA AGC TTA CAG GGA CAC CGG AAT TTT CCC ACT GGA ACT GTT CCC AAA TGG GAT
Val Ser Ser Leu Gln Gly His Arg Asn Phe Pro Thr Gly Thr Val Pro Lys Trp Asp

1145 1160 1175 1190
AGC CAC ATC AGA GCT GCC CTT TCC ATT GAG CGG AGG AAG AAG CGC TCT ACT GGG GTC
Ser His Ile Arg Ala Ala Leu Ser Ile Glu Arg Arg Lys Lys Arg Ser Thr Gly Val

1205 1220 1235 1250
TTG CTG CCT CTG CAG AAC AAC GAG CTT CCT GGG GCA GAA TAC CAG TAT AAA AAG GAT
Leu Leu Pro Leu Gln Asn Asn Glu Leu Pro Gly Ala Glu Tyr Gln Tyr Lys Lys Asp

1265 1280 1295 1310
GAG GTG TGG GAG GAG AGA AAG CCT TAC AAG ACC CTT CAG GCT CAG GCC CCT GAA AAG
Glu Val Trp Glu Glu Arg Lys Pro Tyr Lys Thr Leu Gln Ala Gln Ala Pro Glu Lys

1325 1340 1355 1370
AGT AAG AAT AAA AAG AAA CAG AGA AAG GGG CCT CAT CGG AAG AGC CAG ACG CTC CAA
Ser Lys Asn Lys Lys Gln Arg Lys Gly Pro His Arg Lys Ser Gln Thr Leu Gln

1385 1400 1415
TIT GAT GAG CAG ACC CTG AAA AAG GCA AGG AGA AAG CAG TGG ATT GAA CCT CGG AAT
Phe Asp Glu Gln Thr Leu Lys Lys Ala Arg Arg Lys Gln Trp Ile Glu Pro Arg Asn

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FIGURE 11 (Continued)

1430 1445 (377) 1460 1475
TGC GCC AGG AGA TAC CTC AAG GTC GAC TTT GCA GAT ATT GGC TGG AGT GAA TGG ATT
Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser Glu Trp Ile

1490 1505 1520 1535
ATC TCC CCC AAG TCC TTT GAT GCC TAT TAT TGC TCT GGA GCA TGC CAG TTC CCC ATG
Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser Gly Ala Cys Gln Phe Pro MET

1550 1565 1580 1595
CCA AAG TCT TTG AAG CCA TCA AAT CAT GCT ACC ATC CAG AGT ATA GTG AGA GCT GTG
Pro Lys Ser Leu Lys Pro Ser Asn His Ala Thr Ile Gln Ser Ile Val Arg Ala Val

1610 1625 1640 1655
GGG GTC GTT CCT GGG ATT CCT GAG CCT TGC TGT GTA CCA GAA AAG ATG TCC TCA CTC
Gly Val Val Pro Gly Ile Pro Glu Pro Cys Cys Val Pro Glu Lys MET Ser Ser Leu

1670 1685 1700
AGT ATT TTA TTC TTT GAT GAA AAT AAG AAT GTA GTG CTT AAA GTA TAC CCT AAC ATG
Ser Ile Leu Phe Phe Asp Glu Asn Asn Val Val Leu Lys Val Tyr Pro Asn MET

1715 1730 (472) 1746 1756 1766 1776
ACA GTA GAG TCT TGC GCT TGC AGA TAACCTGGCA AAGAACTCAT TTGAAATGCTT AATTCAATCT
Thr Val Glu Ser Cys Ala Cys Arg

1786
CTAGAGTCGA CGGAATTG